Figure 1

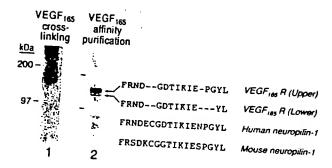


Figure 2A



Figure 2B



Land Control of

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Figure 4

# Com arative Deduced Amino Acia Sequences of Human VEGF<sub>165</sub>R/NP and VEGF<sub>165</sub>R/NP-1

VEGF <sub>IM</sub> R/NP-1	l	MERGIPULCAV-DADVLA-PAGAFR-MOKCGDTIKIESPGY	<b>5</b> 0
NP-	2 5 <sup>-</sup>	I TSPGYPOCHASISTERNANINIADNGESAAYVI-WEDNOHESIEXHOCKYOF I VOYADCHOCHURHRINIADNGESAANOCHURSHGYDGETI I VOYADCHACHURHRINIADNGESAANO	00
NP-	2 10 <sup>.</sup> 1	I IZIRDGOSESADLLGKHCGNIAPPTIISSGSMLYIKFTSDYARQGAGFSL 1 VZVFDGENENGHFRGKFCGKIAPPPVVSSGPFLFIKFVSDYETHGAGFSI	50
NP-:	2 15: 1	RYZIFKTGSZDCSKNFTSPNGTIESPGFPEKYPHN-LDCTFTIL-AKPKM 2 RYZIFKRGPE-CSQNYTTPSGVIKSPGFPEKYP-NSLECTY-IVFA-PKM	0 <b>0</b>
NP-1	2 201 1	-EIILQFLIFDLEHDPLQVGEGD-CKYDWLDIWDGIFHVGPLIGKYCG 2: SEIILEFESFDLEPDSNPPG-GMFCRYDRLEIWDGFFDVGPHIGRYCG	50
NP-1	2 251 1	TKTPSELRSSTGILSLTEHTDMAVAKDGESARYYLVHQEPL-ENEQCNVP 30 QKTPGRIRSSSGILSMVFYTDSALAKEGFSANYS-VLQSSVSZDFKCMEA	00
NP-1	2 301 I	LGMESGRIANEQISASSTYSDGRWTPQQSRLHGDDNGWTPNLDSNKEYLQ 38 LGMESGEIHSDQITASSQYSTN-WSAERSRLNYPENGWTPGEDSYREWIQ	:0
NP-1	2 351 I	VDLRELTMETATATQGAISRETQNGYYVKSYKLEVSTNGEDWMYYRH 40 VDLGLEREVTAVGTQGAISKETKKKYYVKTYKIDVSSNGEDWITIKE	0:
NP-1	2 401 I	GKNHK-V-FQAN-NEATEVVLNKUHAPBETRFVRIRPQTWHSGIAUR 45 G-N-KPVLFQGNTNP-TDVVVAVFPKPLITRFVRIKPATWETGISMR	0
NP-2 NP-1		LELFGGRVTDAPCSHMLGMLSGLIADSQISASSTQEYL-WSPSAARLVSS 50 FEVYGCKITDYPCSGMLGHVSGLISDSQIT-SSNQGDRHWNPSHIRLVTS	
NP-2 NP-1		RSGWF-PRIPQAQPGEEWLQVDLGTPKTVKGVIIQGARGGDSITAVE 55 RSGWALPP-A-PHSYINEWLQIDLGEEKIVRGIIIQGGKHRENKV-	
NP-2 NP-1		ARAFYRKEKYSYSLNGKDWEYIQDPRTQQPRLFEGNMHYDTPDIRRED 60FMRKEKIGYSNNGSDWKMIMDDSKRKAKSFEGNNNYDTPEURTF-	
NP-2 NP-1		PIPAQYVRVYPERWSPAGI-GMRLEVLGCOWTDSKPTVETLGP 65 PALSTRFIRIYPERATHGGLGLRMELLGCEVEAPTAGP	
NP-2 NP-1		TVKSEETTTPYFTEEEATECGENC-SFE-DDKDLQLP- 70 TTPMGMLVDECDDDQANCHSGTGDDFQLTGGTTVLATEKPT	
NP-2 NP-1		SGFNCUFDFLSEPCGWMYD-HAKWLRTT 75 VIDSTIQSEFPTYGFNCEFGNGSHKTFCHWEHDNHVQLKWSVL-T-	
NP-2 NP-1		WASSSSPN-DRTFPDDRHFLRLQSDS-QREGQYARLISPPVHLPRSPVCM 80SKTGPIQDHTG-DG-NFIYSQADENQK-GKVARLVSPVVYSQNSAHCM	
NP-2 NP-1	801	EFQYQATGGRGVALQVVREASQESKLLWV-IREDQGGEWKHGR 85 TFWYHMSGSHVGTLR-VKLRYQKPEEYDQLVWMAIGH-QGDHWKEGR	0
NP-2 NP-1		IILP-SYDMEYQ-IVFEGVIGKGRSGEIAIDDIRISTOVPLENCME 90 VLLHKSLKL-YQVI-FEGEIGKGNLGGIAVDDISINNHISQEDCAK	
NP-1		PISAFAGENFKVDIPEIHERE-GYEDEIDDEYEVDWSNSSSATSGS 95 PADLDKKNPEIKIDETGSTPGYEGEGEGDK-NISRKP-GN	
NP-2 NP-1		GAPSTDREKSWLYTLDPILITIIAMSSLGVLLGATCAGLLLYCTCSYSGL 1000 VLRTLDPILITIIAMSALGVLLGAVC-GVVLYCACWHNGM	כ
NP-2 NP-1	1001	SSRSCTTLENYNFELYDGLKHKVKNNHQHCCSEA 1038 SERNLSALENYNFELVDGVKLK-KOKENTQSTYSEAN	

Figure 5

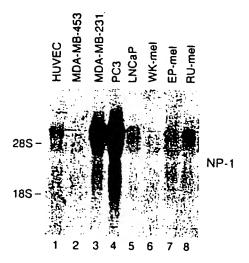


Figure 6

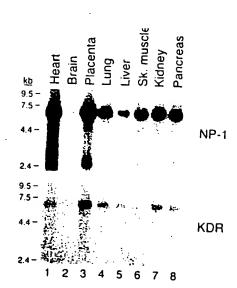




Figure 7A

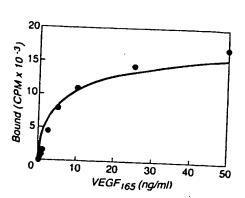


Figure 7B

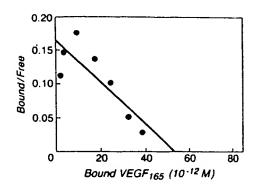


Figure 8

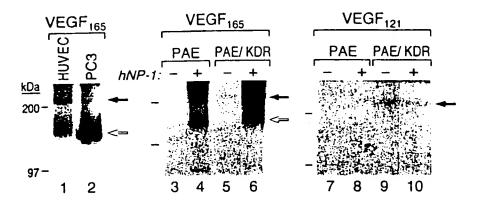


Figure 9

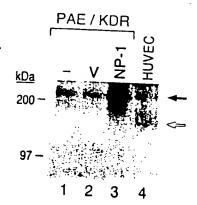
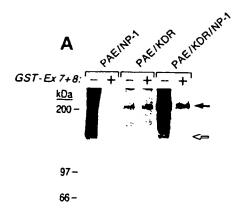
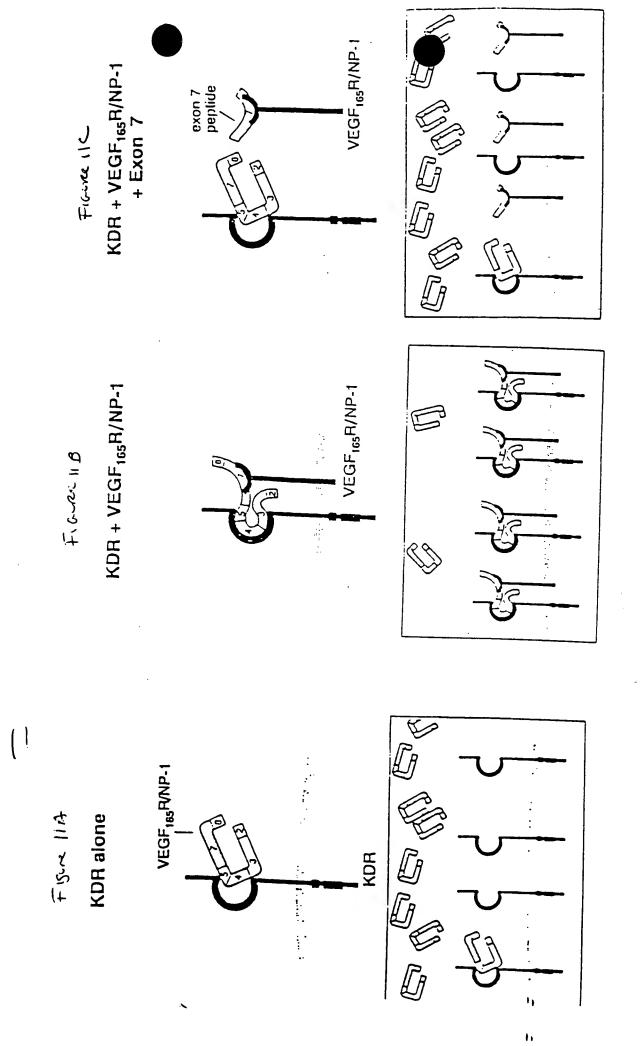


Figure 10





Human Neuropilin-2 amino acid sequence:

MEMFPLTWVFLALYFSRHQVRGQPDPPCGGRLNSKDAGYITSPGYPQDYPSHQN CEWIVYAPEPNCKIVLNFNPHFEIEKHDCKYDFIEIRDGDSESADLLGKHCGNIAPP TIISSGSMLYIKFTSDYARQGAGFSLRYEIFKTGSEDCSKNFTSPNGTIESPGFPEK YPHNLDCTFTILAKPKMEIILQFLIFDLEHDPLQVGEGDCKYDWLDIWDGIPHVGPL IGKYCGTKTPSELRSSTGILSLTFHTDMAVAKDGFSARYYLVHQEPLENFQCNVP LGMESGRIANEQISASSTYSDGRWTPQCSRLHGDDNGWTPNLDSNKEYLQVDLR FLTMLTAIATQGAISRETQNGYYVKSYKLEVSTNGEDWMVYRHGKNHKVFQANN DATEVVLNKLHAPLLTRFVRIRPQTWHSGIALRLELFGCRVTDAPCSNMLGMLS GLIADSQISASSTQEYLWSPSAARLVSSRSGWFPRIPQAQFGEEWLQVDLGTPK TVKGVIIQGARGGDSITAVEARAFVRKFKVSYSLNGKDWEYIQDPRTQQPKLFEG NMHYDTPDIRRFDPIPAQYVRVYPERWSPAGIGMRLEVLGCDWTDSKPTVETLG PTVKSEETTTPYPTEEEATECGENCSFEDDKDLGLPSGFNCNFDFLEEPCGWMYD HAKWLATTWASSSSPNDRTFPDDRNFLRLQSDSQREGQYARUSPPVHLPRSPV CMEFQYQATGGRGVALQVVREASCESKLLWVIREDQGGEWKHGRIILPSYDMEYQ IVFEGVIGKGRSGEIAIDDIRISTDVPLENCMEPISAFAGENFKVDIPEIHEREGYED EIDDEYEVDWSNSSSATSGSGAPSTDKEKSWLYTLDPILITIIAMSSLGVLLGAT CAGLLLYCTCSYSGLSSRSCTTLENYNFELYDGLKHKVKMNHQKCCSEA\*

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		aagetgteea	<b>y</b> ctt		3404

774 283 756 765 ATG GAG AGG GGG CTG CCG CTC CTC TGC GCC GTG CTC GCC CTC GTC CTC GCC CCG M E R G L P L L C A V I A L V L A 328 319 310 GCC GGC GCT TTT CGC AAC GAT AAA TGT GGC GAT ACT ATA AAA ATT GAA AGC CCC A F R IN D K C G D T I K I E S P 373 GGG TAC CTI ACA TCT CCI GGT TAT CCT CAT TCT TAT CAC CCA AGT GAA AAA TGC GY L T S P G Y P H S Y H P GAA TGG CTG ATT CAG GCT CCG GAC CCA TAC CAG AGA ATT ATG ATC AAC TTC AAC E W L I Q A P D P Y Q R I M I N F N 499 490 481 472 CCT CAC TTC GAT TTG GAG GAC AGA GAC TGC AAG TAT GAC TAC GTG GAA GTG TTC LEDRDCKYUYVCVF 553 544 535 526 GAT GGA GAN AAT GAA AAT GGA CAT TIT NGG GGA AAG TIC TGT GGA AAG ATA GCC ENENGHFRGK + CGK 571 CCT CCT CCT GTT GTG TCT TCA GGG CCA TTT CTT TIT ATC AAA TTI GTC TCT GAC P P P V V S S G P F L F J K F V 661 652 634 643 TAC GAA ACA CAT GGT GCA GGA TTT TCC ATA CGT TAT GAA ATT TIC AAG AGA GGT R Y E YETHGAGFSI 715 706 697 688 CCT GAA TGT TCC CAG AAC TAC ACA ACA CCT AGT GGA GTG ATA AAG TCC CCC GGA Y T T P S G V I K S P G N 760 751 TTC CCT GAA AAA TAT CCC AAC AGC CTT GAA TGC ACT TAT ATT GTC TTT GCG CCA FP & K Y P N S L E C T Y I V F A P 805 ANG ATG TCA GAG ATT ATC CTG GAA TTI GAA AGC TTT GAC CTG GAG CCT GAC ICA MSEIILEFES F D L E P 859 868 850 AAT CCT CCA GGG GGG ATG TTC TGT CGC TAC GAC CGG CTA GAA ATC TGG GAT GGA N P P G G M F C R Y D R L F I W D G 931 913 922 904 TIC CCT GAT GIT GGC CCT CAC ATT GGG CGT TAC TGT GGA CAG AAA ACA CCA GGT POVGPHIGRYCGQKTPG 976 967 958 CGA ATC CGA TCC TCA TCG GGC ATT CTC TCC ATG GTT TTT TAC ACC GAC AGC GCG RIRSSSGILSMVFYT

ATA GCA AAN GAA GGT TTC TCA GCA AAC TAC AGT GTC TTG CAG AGC AG TC TCA IAKEGESANYSVLQSSVS GAA GAT TTC AAA TGT ATG GAA GCT CTG GGC ATG GAA TCA GGA GAA ATT CAT TCT S ALGHE GAC CAG ATC ACA GCT TCT TCC CAG TAT AGC ACC AAC TGG TCT GCA GAG CGC TCC DQITASSQYSTNWSAC CGC CTG AAC TAC CCT GAG AAT GGG TGG ACT CCC GGA GAG GAT TCC TAC CGA GAG LNYPENGWTPGEDSYRE TGG ATA CAG GTA GAC TIG GGC CTT CTG CGC TTT GTC ACG GCT GTC GGG ACA CAG R F V T A V G T Q WIQVDLGLL GGC GCC ATT TCA AAA GAA ACC AAG AAG AAA TAT TAT GTC AAG ACT TAC AAG ATC K K K Y Y V K T Y K I GAISKET GAC GTT AGC TCC AAC GGG GAA GAC TGG ATC ACC ATA AAA GAA GGA AAC AAA CCT SSNG Ε DWITIKEGNKP GIT CTC TIT CAG GGA AAC ACC AAC CCC ACA GAT GTT GTG GTT GCA GTA TTC CCC V L F Q G N T N P T O V V A V F P AAA CCA CTG ATA ACT CGA TTT GTC CGA ATC AAG CCI GCA ACT TGG GAA ACT GGC K P L I T R F V R I K P A T W E T G ATA TCI ATG AGA TTT GAA GTA TAC GGT TGC AAG ATA ACA GAT TAT CCT TGC TCT SMRFEVYGCKITOY61PC62S GGA ATG TYG GGT ATG GTG TCT GGA CTY ATT TCT GAC TCC CAG ATC ACA TCA TCC M L G M V S LISOSQITSS G AAC CAA GGG GAC AGA AAC TGG ATG CCT GAA AAC ATC CGC CTG GTA ACC AGT CGC QGORNWMPENIRLVTSR TCT GGC TGG GCA CTT CCA CCC GCA CCT CAT ICC TAC ATC AAT GAG TGG CTC CAA S G W A L P P A P H S Y 1 N E W L Q ANA GAC CTG GGG GAG GAG ANG ATC GTG AGG GGC ATC ATC ATT CAG GGT GGG AAG I D L G E C K I V R G I I I Q G G K CAC CGA GAG AAC MAG GTG TTC ATG AGG MAG TTC AAG ATC GGG TAC AGC MAC AAC

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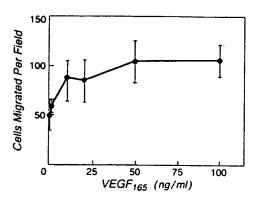
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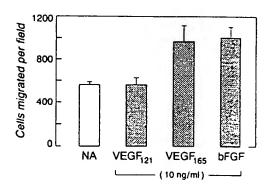
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2623 263 2641 2650 2659 2668
ATT GCT GTG GAT GAC ATT AGT ATT AAC AAC CAC ATT TCA CAA GAA TGT GCA AVOOISINNHISQEOC 2686 2695 2722 2704 2713 AAA CCA GCA GAC CTG GAT AAA AAG AAC CCA GAA ATT AAA ATT GAT GAA ACA GGG K P A D L D K K' N P E I K I D E T G 2749 2758 2740 AGC ACG CCA GGA TAC GAA GGT GAA GGA GAA GGT GAC AAG AAC ATC TCC AGG AAG STPGYEGEGOKNISRK 2794 2803 2812 CCA GGC AAT GTG TTG AAG ACC TTA GAT CCC ATC CTC ATC ACC ATC ATA GCC ATG PGNVLKTLOPLITHITIAM 2857 2866 2875 2848 AGT GCC CTG GGG GTC CTC CTG GGG GCT GTC TGT GGG GTC GTG CTG TAC TGT GCC SALGVLLGAVCGVVLYCA 2902 2911 2920 7929 2938 TGT TGG CAT AAT GGG ATG TCA GAA AGA AAC TTG TCT GCC CTG GAG AAC TAT AAC HI CN + G M S E R N L S A L E N Y N 2965 2974 2956 TIT GAA CTT GTG GAT GGT GTG AAG TIG AAA AAA GAC AAA CTG AAT ACA CAG AGT F C L V D G V K L K X D K L N T Q S ACT TAT TCG GAG GCA TGA 3' (SEX TO NO:1) Y S E AJ. (SEG ID NO:4)

Figure 15A

Figure 15B





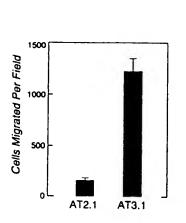


Figure 16A

Figure 16B

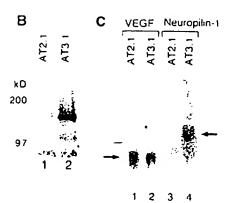


Figure 16C

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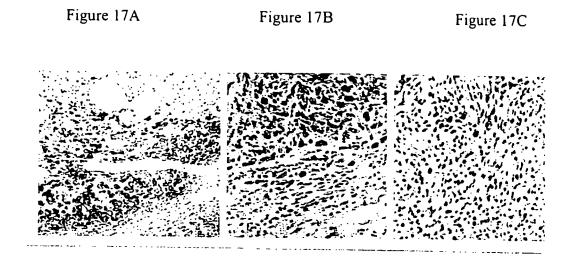
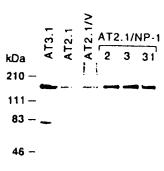
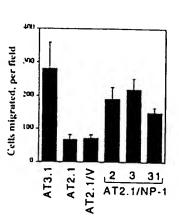


Figure 18A

Figure 18B





β-actin

NP-2

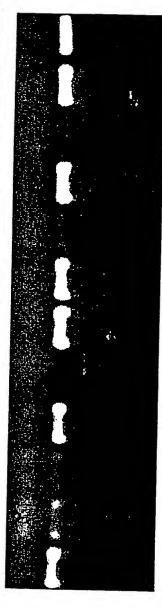
NP-1

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RU EP WK PC3 **LNCaP** 231 **U87 T47** SK Jurkat **HUVEC RPE** 

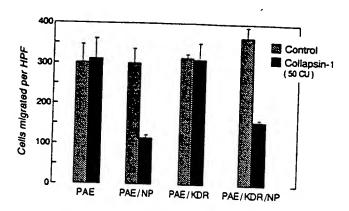


Figure 21A

